

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/589,510

DATE: 06/19/2000
TIME: 12:11:54

Input Set : A:\1121SEQLIST.TXT
Output Set: N:\CRF3\06192000\I589510.raw

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4 <110> APPLICANT: Mahajan, Pramod B.
6 <120> TITLE OF INVENTION: Maize Orthologues of Bacterial RuvB:
7   cDNAs and Uses Thereof
9 <130> FILE REFERENCE: 1121
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/589,510
C--> 11 <141> CURRENT FILING DATE: 2000-06-07
11 <150> PRIOR APPLICATION NUMBER: US 60/144,112
12 <151> PRIOR FILING DATE: 1999-07-16
14 <160> NUMBER OF SEQ ID NOS: 11
16 <170> SOFTWARE: FastSeq for Windows Version 3.0
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 1845
20 <212> TYPE: DNA
21 <213> ORGANISM: Zea mays
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (85)...(1449)
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28   gacccacgcg tcgcccaccc cccgccccca aattttggca gctccacaga aacagagagc   60
29   gcataaccgg cgttggtggc ggcgatg agg atc gag gag gtg cag tcg acc   111
30                                     Met Arg Ile Glu Glu Val Gln Ser Thr
31                                     1           5
33   tcg aag aag cag cgc atc gcc acc cac acc cac atc aag gga ctc ggc   159
34   Ser Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly Leu Gly
35   10           15           20           25
37   ctc gac gcc aat ggg atg gcg att gcg ttg gcg gcg ggg ttc gtg ggc   207
38   Leu Asp Ala Asn Gly Met Ala Ile Ala Leu Ala Ala Gly Phe Val Gly
39   30           35           40
41   cag tcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg att cgc   255
42   Gln Ser Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met Ile Arg
43   45           50           55
45   cag aaa aag atg gcc ggc cgc gcg gtg ctc ctt gtg ggt ccg ccc gcc   303
46   Gln Lys Lys Met Ala Gly Arg Ala Val Leu Leu Val Gly Pro Pro Ala
47   60           65           70
49   acg ggc aag acg gcg cta gcg ctc ggc ata gcc cag gag ctc ggc agc   351
50   Thr Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu Gly Ser
51   75           80           85
53   aag gtc cct ttc tgc cct atg gta gga tca gaa gtg tac tcc tcg gag   399
54   Lys Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser Ser Glu
55   90           95           100           105
57   gtc aag aaa act gag gtg ctg atg gaa aat ttc cgt aga gct ata ggt   447
58   Val Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala Ile Gly
59   110           115           120
61   ttg cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt act gaa   495
62   Leu Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val Thr Glu
63   125           130           135
65   ctt tcc cca gaa gag gct gag agt aca act ggt gga tat gca aaa agc   543

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66  Leu Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala Lys Ser
67      140      145      150
69  att agc cat gta atc atc agc tta aag act gtt aaa ggg act aag caa      591
70  Ile Ser His Val Ile Ile Ser Leu Lys Thr Val Lys Gly Thr Lys Gln
71      155      160      165
73  ctg aag tta gat tct tca att tat gat gct ctg atc aag gaa aag gtg      639
74  Leu Lys Leu Asp Ser Ser Ile Tyr Asp Ala Leu Ile Lys Glu Lys Val
75      170      175      180      185
77  gca gtg ggt gat gtt ata tac att gaa gca aat agt gga gca gtg aaa      687
78  Ala Val Gly Asp Val Ile Tyr Ile Glu Ala Asn Ser Gly Ala Val Lys
79      190      195      200
81  aga gtt ggt aga tgt gat tct ttt gct aca gaa tac gat ctt gaa gct      735
82  Arg Val Gly Arg Cys Asp Ser Phe Ala Thr Glu Tyr Asp Leu Glu Ala
83      205      210      215
85  gaa gaa tat gtt cct atc ccc aaa ggt gaa gtc cat aag aaa aaa gaa      783
86  Glu Glu Tyr Val Pro Ile Pro Lys Gly Glu Val His Lys Lys Lys Glu
87      220      225      230
89  ata gtg cag gat gtc aca ctt cat gac ctt gat gca gca aat gct cag      831
90  Ile Val Gln Asp Val Thr Leu His Asp Leu Asp Ala Ala Asn Ala Gln
91      235      240      245
93  cca caa ggt ggc caa gat att ttg tcc ctt atg ggc cag atg atg aaa      879
94  Pro Gln Gly Gly Gln Asp Ile Leu Ser Leu Met Gly Gln Met Met Lys
95      250      255      260      265
97  cca cga aag act gaa atc acc gaa aaa cta cgc caa gaa att aat aag      927
98  Pro Arg Lys Thr Glu Ile Thr Glu Lys Leu Arg Gln Glu Ile Asn Lys
99      270      275      280
101  gtg gta aat aga tat atc gat gaa gga att gca gag ctt gta cct ggt      975
102  Val Val Asn Arg Tyr Ile Asp Glu Gly Ile Ala Glu Leu Val Pro Gly
103      285      290      295
105  gtt tta ttc att gac gag gtc cac atg ttg gat atc gaa tgt ttt tct      1023
106  Val Leu Phe Ile Asp Glu Val His Met Leu Asp Ile Glu Cys Phe Ser
107      300      305      310
109  tat ctt aac cgt gca ttg gag agc cca tta tca cca att gtg ata ctt      1071
110  Tyr Leu Asn Arg Ala Leu Glu Ser Pro Leu Ser Pro Ile Val Ile Leu
111      315      320      325
113  gct acg aat agg gga ata tgt aat gta aga gga act gat atg aca agt      1119
114  Ala Thr Asn Arg Gly Ile Cys Asn Val Arg Gly Thr Asp Met Thr Ser
115      330      335      340      345
117  cca cat ggt ata cca gtg gat ctt cta gat agg ttg gtg att att cgg      1167
118  Pro His Gly Ile Pro Val Asp Leu Leu Asp Arg Leu Val Ile Ile Arg
119      350      355      360
121  aca gag aca tat ggc cct act gag atg ata cag ata ttg gct atc cga      1215
122  Thr Glu Thr Tyr Gly Pro Thr Glu Met Ile Gln Ile Leu Ala Ile Arg
123      365      370      375
125  gca caa gtg gag gac att gat atg gat gaa gaa agt ctt gct tat tta      1263
126  Ala Gln Val Glu Asp Ile Asp Met Asp Glu Glu Ser Leu Ala Tyr Leu
127      380      385      390
129  ggc gag atc gga cag cag aca tct tta aga cat gct att caa ttg ata      1311
130  Gly Glu Ile Gly Gln Gln Thr Ser Leu Arg His Ala Ile Gln Leu Ile

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131      395      400      405      1359
133 tca cct gcc agc gtg gtc tca aag act aat gga aga gag aaa ata tgc
134 Ser Pro Ala Ser Val Val Ser Lys Thr Asn Gly Arg Glu Lys Ile Cys
135 410      415      420      425      1407
137 aag gct gat ctc gag gaa gtc agt ggg ctc tat ttg gat gcc aaa tcc
138 Lys Ala Asp Leu Glu Glu Val Ser Gly Leu Tyr Leu Asp Ala Lys Ser
139      430      435      440      1449
141 tcg gct cgg ctg ctc cag gag caa caa gaa aga tac atc acc
142 Ser Ala Arg Leu Leu Gln Glu Gln Glu Arg Tyr Ile Thr
143      445      450      455
145 tagatttgga tcacctgtcg tggaagtctc gaagagaatg tagttgccag ctcgaaagtc 1509
146 atctagttaa ttgatctgct tcacaggtct tggagcgagc acatttcggg ggggacggct 1569
147 tgaattttgc agtgccctgct tgtgttagtg tccagagaag acttggtacc ggcattattgc 1629
148 ctgttcacgc actgttcgct gattagattg gtcaccgggtg caggaattgc cgtgtgtgtt 1689
149 ttttatcttg ctcatcggtg tccggaatct gtgcctccac gggttgtatt ggcccgaacc 1749
150 ctatctttgt aaccatggat aatggatagc attcttacag aatgcaactt gcatggcttt 1809
151 wttwaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 1845
153 <210> SEQ ID NO: 2
154 <211> LENGTH: 455
155 <212> TYPE: PRT
156 <213> ORGANISM: Zea mays
158 <400> SEQUENCE: 2
159 Met Arg Ile Glu Glu Val Gln Ser Thr Ser Lys Lys Gln Arg Ile Ala
160 1 5 10 15
161 Thr His Thr His Ile Lys Gly Leu Gly Leu Asp Ala Asn Gly Met Ala
162 20 25 30
163 Ile Ala Leu Ala Ala Gly Phe Val Gly Gln Ser Ala Ala Arg Glu Ala
164 35 40 45
165 Ala Gly Leu Ala Val Asp Met Ile Arg Gln Lys Lys Met Ala Gly Arg
166 50 55 60
167 Ala Val Leu Leu Val Gly Pro Pro Ala Thr Gly Lys Thr Ala Leu Ala
168 65 70 75 80
169 Leu Gly Ile Ala Gln Glu Leu Gly Ser Lys Val Pro Phe Cys Pro Met
170 85 90 95
171 Val Gly Ser Glu Val Tyr Ser Ser Glu Val Lys Lys Thr Glu Val Leu
172 100 105 110
173 Met Glu Asn Phe Arg Arg Ala Ile Gly Leu Arg Ile Lys Glu Asn Lys
174 115 120 125
175 Glu Val Tyr Glu Gly Glu Val Thr Glu Leu Ser Pro Glu Ala Glu
176 130 135 140
177 Ser Thr Thr Gly Gly Tyr Ala Lys Ser Ile Ser His Val Ile Ile Ser
178 145 150 155 160
179 Leu Lys Thr Val Lys Gly Thr Lys Gln Leu Lys Leu Asp Ser Ser Ile
180 165 170 175
181 Tyr Asp Ala Leu Ile Lys Glu Lys Val Ala Val Gly Asp Val Ile Tyr
182 180 185 190
183 Ile Glu Ala Asn Ser Gly Ala Val Lys Arg Val Gly Arg Cys Asp Ser
184 195 200 205
185 Phe Ala Thr Glu Tyr Asp Leu Glu Ala Glu Glu Tyr Val Pro Ile Pro

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186          210          215          220
187 Lys Gly Glu Val His Lys Lys Lys Glu Ile Val Gln Asp Val Thr Leu
188 225          230          235          240
189 His Asp Leu Asp Ala Ala Asn Ala Gln Pro Gln Gly Gly Gln Asp Ile
190          245          250          255
191 Leu Ser Leu Met Gly Gln Met Met Lys Pro Arg Lys Thr Glu Ile Thr
192          260          265          270
193 Glu Lys Leu Arg Gln Glu Ile Asn Lys Val Val Asn Arg Tyr Ile Asp
194          275          280          285
195 Glu Gly Ile Ala Glu Leu Val Pro Gly Val Leu Phe Ile Asp Glu Val
196          290          295          300
197 His Met Leu Asp Ile Glu Cys Phe Ser Tyr Leu Asn Arg Ala Leu Glu
198          305          310          315          320
199 Ser Pro Leu Ser Pro Ile Val Ile Leu Ala Thr Asn Arg Gly Ile Cys
200          325          330          335
201 Asn Val Arg Gly Thr Asp Met Thr Ser Pro His Gly Ile Pro Val Asp
202          340          345          350
203 Leu Leu Asp Arg Leu Val Ile Ile Arg Thr Glu Thr Tyr Gly Pro Thr
204          355          360          365
205 Glu Met Ile Gln Ile Leu Ala Ile Arg Ala Gln Val Glu Asp Ile Asp
206          370          375          380
207 Met Asp Glu Glu Ser Leu Ala Tyr Leu Gly Glu Ile Gly Gln Gln Thr
208          385          390          395          400
209 Ser Leu Arg His Ala Ile Gln Leu Ile Ser Pro Ala Ser Val Val Ser
210          405          410          415
211 Lys Thr Asn Gly Arg Glu Lys Ile Cys Lys Ala Asp Leu Glu Glu Val
212          420          425          430
213 Ser Gly Leu Tyr Leu Asp Ala Lys Ser Ser Ala Arg Leu Leu Gln Glu
214          435          440          445
215 Gln Gln Glu Arg Tyr Ile Thr
216          450          455
218 <210> SEQ ID NO: 3
219 <211> LENGTH: 1912
220 <212> TYPE: DNA
221 <213> ORGANISM: Zea mays
223 <220> FEATURE:
224 <221> NAME/KEY: CDS
225 <222> LOCATION: (94)...(1458)
227 <400> SEQUENCE: 3
228 acccagcggt ccgcaaattt gttgcggcgg gagagccgga gaggaggcag ctccacagaa 60
229 acagagagcg cataaccggc ggcgttggcg gcg atg agg atc gag gag gtg cag 114
230          Met Arg Ile Glu Glu Val Gln
231          1          5
233 tcg acc tcg aag aag cag cgc atc gcc acc cac acc cac atc aag gga 162
234 Ser Thr Ser Lys Lys Gln Arg Ile Ala Thr His Thr His Ile Lys Gly
235          10          15          20
237 ctc ggc ctc gac gcc aat ggg atg gcg att gcg ttg gcg gcg ggg ttc 210
238 Leu Gly Leu Asp Ala Asn Gly Met Ala Ile Ala Leu Ala Ala Gly Phe
239          25          30          35

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241	gtg ggc cag gcg gcg gcg cgc gag gcg gcc ggg ctg gcg gtc gac atg	258
242	Val Gly Gln Ala Ala Ala Arg Glu Ala Ala Gly Leu Ala Val Asp Met	
243	40 45 50 55	
245	att cgc cag aag aag atg gcc ggc cgc gcg gtg ctc ctt gcg ggt ccg	306
246	Ile Arg Gln Lys Lys Met Ala Gly Arg Ala Val Leu Leu Ala Gly Pro	
247	60 65 70	
249	ccc gcc acg ggc aag acg gcg cta gcg ctc gcc ata gcc cag gag ctc	354
250	Pro Ala Thr Gly Lys Thr Ala Leu Ala Leu Gly Ile Ala Gln Glu Leu	
251	75 80 85	
253	ggc agc aag gtc cct ttc tgt cct atg gta gga tca gaa gtg tac tcc	402
254	Gly Ser Lys Val Pro Phe Cys Pro Met Val Gly Ser Glu Val Tyr Ser	
255	90 95 100	
257	tcg gag gtc aag aaa act gag gtg ctg atg gaa aat ttc cgt aga gct	450
258	Ser Glu Val Lys Lys Thr Glu Val Leu Met Glu Asn Phe Arg Arg Ala	
259	105 110 115	
261	ata ggt ttg cgt ata aag gaa aac aaa gag gtt tat gaa gga gag gtt	498
262	Ile Gly Leu Arg Ile Lys Glu Asn Lys Glu Val Tyr Glu Gly Glu Val	
263	120 125 130 135	
265	act gaa ctt tcc cca gaa gag gct gag agt aca act ggt gga tat gca	546
266	Thr Glu Leu Ser Pro Glu Glu Ala Glu Ser Thr Thr Gly Gly Tyr Ala	
267	140 145 150	
269	aaa agc att agc cat gta atc atc agc tta aag act gtt aaa ggg act	594
270	Lys Ser Ile Ser His Val Ile Ile Ser Leu Lys Thr Val Lys Gly Thr	
271	155 160 165	
273	aag caa ctg aag tta gat tct tca att tat gat gct ctg atc aag gaa	642
274	Lys Gln Leu Lys Leu Asp Ser Ser Ile Tyr Asp Ala Leu Ile Lys Glu	
275	170 175 180	
277	aag gtg gca gtg ggt gat gtt ata tac atc gaa gca aat agt gga gca	690
278	Lys Val Ala Val Gly Asp Val Ile Tyr Ile Glu Ala Asn Ser Gly Ala	
279	185 190 195	
281	gtg aaa aga gtt ggt aga tgt gat tct ttt gct aca gaa tac gat ctt	738
282	Val Lys Arg Val Gly Arg Cys Asp Ser Phe Ala Thr Glu Tyr Asp Leu	
283	200 205 210 215	
285	gaa gct gaa gag tat gtt cct atc ccc aaa ggt gaa gtc cat aag aaa	786
286	Glu Ala Glu Glu Tyr Val Pro Ile Pro Lys Gly Glu Val His Lys Lys	
287	220 225 230	
289	aaa gaa att gtg cag gat gtc aca ctt cat gac ctt gat gca gca aat	834
290	Lys Glu Ile Val Gln Asp Val Thr Leu His Asp Leu Asp Ala Ala Asn	
291	235 240 245	
293	gct cag cca caa ggt ggc caa gat att ttg tcc ctt atg ggc cag atg	882
294	Ala Gln Pro Gln Gly Gly Gln Asp Ile Leu Ser Leu Met Gly Gln Met	
295	250 255 260	
297	atg aaa cca cga aag act gaa atc acc gaa aaa cta cgc caa gaa att	930
298	Met Lys Pro Arg Lys Thr Glu Ile Thr Glu Lys Leu Arg Gln Glu Ile	
299	265 270 275	
301	aat aag gtg gta aat aga tat atc gat gaa gga att gca gag ctt gta	978
302	Asn Lys Val Val Asn Arg Tyr Ile Asp Glu Gly Ile Ala Glu Leu Val	
303	280 285 290 295	
305	cct ggt gtt ttg ttc att gat gag gtc cac atg ttg gat atc gaa tgt	1026

VERIFICATION SUMMARY

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Input Set : A:\1121SEQLIST.TXT

Output Set: N:\CRF3\06192000\I589510.raw

OK L:11 M:270 C: Current Application Number differs, Replaced Current Application No
L:21 M:271 C: Current Filing Date differs, Replaced Current Filing Date